<110> Wang, Danher

<120> GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS

<130> 22488-712

<150> 09/585,599
<151> 2000-06-02

<150> PCT/US01/18238
<151> 2001-06-04

<160> 75

<170> PatentIn version 3.1

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<213> Ebola virus

<400> 1
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<400> 2
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<210> 3
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<212> RNA
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<220>
<223> Modified RNA editing site

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<210>   9
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<213>   Homo sapiens

<400>   9

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gaagcatcca ggaagtcagc ctaaaactgc ttgtaccaat tgctattgta aaaagtgttg     180

ctttcattgc caagtttgtt tcataacaaa agccttaggc atctcctatg gcaggaagaa     240

gcggagacag cgacgaagac ctcctcaagg cagtcagact catcaagttt ctctatcaaa     300

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gcagtaagta gtacatgtaa tgcaacctat acaaatagca atagtagcat tagtagtagc     360

aataataata gcaatagttg tgtggtccat agtaatcata gaatatagga aaatattaag     420

acaaagaaaa atagacaggt taattgatag actaatagaa agagcagaag acagtggcaa     480

tgagagtgaa ggagaaatat cagcacttgt ggagatgggg gtggagatgg ggcaccatgc     540

tccttgggat gttgatgatc tgtagtgcta cagaaaaatt gtgggtcaca gtctattatg     600

gggtacctgt gtggaaggaa gcaaccacca ctctattttg tgcatcagat gctaaagcat     660

atgatacaga ggtacataat gtttgggcca cacatgcctg tgtacccaca gaccccaacc     720

cacaagaagt agtattggta aatgtgacag aaaattttaa catgtggaaa aatgacatgg     780

tagaacagat gcatgaggat ataatcagtt tatgggatca aagcctaaag ccatgtgtaa     840

aattaacccc actctgtgtt agtttaaagt gcactgattt gaagaatgat actaatacca     900

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atgtcagcac agtacaatgt acacatggaa ttaggccagt agtatcaact caactgctgt    1260

taaatggcag tctggcagaa gaagaggtag taattagatc tgccaatttc acagacaatg    1320

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acaatacaag aaaaagtatc cgtatccaga gaggaccagg gagagcattt gttacaatag    1440

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gtactaaagg gtcaaataac actgaaggaa gtgacacaat caccctccca tgcagaataa    1740

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gcaacaatga gtccgagatc ttcagacctg gaggaggaga tatgagggac aattggagaa    1920

gtgaattata taaatataaa gtagtaaaaa ttgaaccatt aggagtagca cccaccaagg    1980

caaagagaag agtggtgcag agagaaaaaa gagcagtggg aataggagct ttgttccttg    2040

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tggctgtgga aagataccta aaggatcaac agctcctggg gatttggggt tgctctggaa      2280

aactcatttg caccactgct gtgccttgga atgctagttg gagtaataaa tctctggaac      2340

agatttggaa taacatgacc tggatggagt gggacagaga aattaacaat tacacaagct      2400

taatacactc cttaattgaa gaatcgcaaa accagcaaga aagaatgaa caagaattat       2460

tggaattaga taaatgggca agtttgtgga attggtttaa cataacaaat tggctgtggt      2520

atataaaatt attcataatg atagtaggag gcttggtagg tttaagaata gttttttgctg     2580

tactttctgt agtgaataga gttaggcagg gatattcacc attatcgttt cagacccacc      2640

tcccaatccc gaggggaccc gacaggcccg aaggaataga agaagaggt ggagagagag        2700

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gccacatacc tagaagaata agacagggct tggaaaggat tttgctataa gatgggtggc      3060

aagtggtcaa aaagtagtgt ggttggatgg cctgctgtaa gggaaagaat gagacgagct      3120

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<220>
<223> Modified IL-2

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ttctacaaag aaaacacagc tacaactgga gcatttactg ctggatttac agatgatttt      180

gaatggaatt aataattaca agaatcccaa actcaccagg atgctcacat ttaagtttta      240

catgcccaag aaggccacag aactgaaaca tcttcagtgt cttgaagaag aactcaaacc      300

tctggaggaa gtgctaaatt tagctcaaag caaaaacttt cacttaagac ccagggactt      360

aatcagcaat atcaacgtaa tagttctgga actaaaggga tctgaaacaa cattcatgtg      420

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acagtctatt atggggtacc tgtgtggaag gaagcaacca ccactctatt ttgtgcatca    180

gatgctaaag catatgatac agaggtacat aatgtttggg ccacacatgc ctgtgtaccc    240

acagacccca acccacaaga agtagtattg gtaaatgtga cagaaaattt taacatgtgg    300

aaaaatgaca tggtagaaca gatgcatgag gatataatca gtttatggga tcaaagccta    360

aagccatgtg taaaattaac cccactctgt gttagtttaa agtgcactga tttgaagaat    420

gatactaata ccaatagtag tagcgggaga atgataatgg agaaggaga gataaaaaac      480

tgctctttca atatcagcac aagcataaga ggtaaggtgc agaaagaata tgcatttttt    540

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ggaccatgta caaatgtcag cacagtacaa tgtacacatg gaattaggcc agtagtatca    780

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aaatggaata acactttaaa acagatagat agcaaattaa gagaacaatt tggaaataat   1080

aaaacaataa tctttaagca gtcctcagga ggggacccag aaattgtaac gcacagtttt   1140

aattgtggag gggaattttt ctactgtaat tcaacacaac tgtttaatag tacttggttt   1200

aatagtactt ggagtactaa agggtcaaat aacactgaag gaagtgacac aatcaccctc   1260

ccatgcagaa taaaacaaat tataaacatg tggcaggaag taggaaaagc aatgtatgcc   1320

cctcccatca gtggacaaat tagatgttca tcaaatatta cagggctgct attaacaaga   1380

gatggtggta atagcaacaa tgagtccgag atcttcagac ctggaggagg agatatgagg   1440
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gcacccacca aggcaaagag aagagtggtg cagactagtg cagtgggaat aggagctttg 1560

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tctggaaaac tcatttgcac cactgctgtg ccttggaatg ctagttggag taataaatct 1860

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acaagcttaa tacactcctt aattgaagaa tcgcaaaacc agcaagaaaa gaatgaacaa 1980

gaattattgg aattagataa atgggcaagt ttgtggaatt ggtttaacat aacaaattgg 2040

ctgtggtata taaaattatt cataatgata gtaggaggct tggtaggttt aagaatagtt 2100

tttgctgtac tttctgtagt gaatagagtt aggcagggat attcaccatt atcgtttcag 2160

acccacctcc caatcccgag gggacccgac aggcccgaag gaatagaaga agaaggtgga 2220

gagagagaca gagacagatc cattcgatta gtgaacggat ccttagcact tatctggtaa 2280

<210> 17
<211> 1496
<212> DNA
<213> Artificial sequence

<220>
<223> Full length Gag

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tatgggcaag cagggagcta gaacgactac aaccatccct tcagacagga tcagaagaac 180

ttagatcatt atataataca gtagcaaccc tctattgtgt gcatcaaagg atagagataa 240

aagacaccaa ggaagcttta gacaagatag aggaagagca aaacaaaagt aagaaaaaag 300

cacagcaagc agcagctgac acaggacaca gcagtcaggt cagccaaaat taccctatag 360

tgcagaacat ccaggggcaa atggtacatc aggccatatc acctagaact ttaaatgcat 420

gggtaaaagt agtagaagag aaggctttca gcccagaagt aatacccatg ttttcagcat 480

tatcagaagg agccacccca caagatttaa acaccatgct aaacacagtg gggggacatc 540

aagcagccat gcaaatgtta aaagagacca tcaatgagga agctgcagaa tgggatagag 600

tacatccagt gcatgcaggg cctattgcac caggccagat gagagaacca aggggaagtg 660

acatagcagg aactactagt acccttcagg aacaaatagg atggatgaca ataatccac 720

ctatcccagt aggagaaatt tataaaagat ggataatcct gggattaaat aaaatagtaa    780

gaatgtatag ccctaccagc attctggaca taagacaagg accaaaagaa cctttttagag   840

actatgtaga ccggttctat aaaactctaa gagccgagca agcttcacag gaggtaaaaa    900

attggatgac agaaaccttg ttggtccaaa atgcgaaccc agattgtaag actattttaa    960

aagcattggg accagcggct acactagaag aaatgatgac agcatgtcag ggagtaggag    1020

gacccggcca taaggcaaga gttttggctg aagcaatgag ccaagtaaca aatacagcta    1080

ccataatgat gcagagaggc aattttagga accaaagaaa gatggttaag tgtttcaatt    1140

gtggcaaaga agggcacaca gccagaaatt gcagggcccc taggaaaaag ggctgttgga    1200

aatgtggaaa ggaaggacac caaatgaaag attgtactga gagacaggct aattttttag    1260

ggaagatctg gccttcctac aagggaaggc cagggaattt tcttcagagc agaccagagc    1320

caacagcccc accatttctt cagagcagac cagagccaac agccccacca gaagagagct    1380

tcaggtctgg ggtagagaca caactccccc tcagaagca ggagccgata gacaaggaac     1440

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<212> PRT
<213> Human immunodeficiency virus type 1

<400> 18

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Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
                20                  25                  30


His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Leu Gln Pro Ser Leu
            35                  40                  45


Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn Thr Val Ala Thr
        50                  55                  60


Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp Thr Lys Glu Ala
65                  70                  75                  80


Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys Lys Lys Ala Gln
                85                  90                  95


Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val Ser Gln Asn Tyr
            100                 105                 110

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Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His Gln Ala Ile Ser
    115                 120                 125

Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu Lys Ala Phe
    130                 135                 140

Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala Thr
145                 150                 155                 160

Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln Ala
                165                 170                 175

Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu Trp
                180                 185                 190

Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln Met
                195                 200                 205

Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln
    210                 215                 220

Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly Glu
225                 230                 235                 240

Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg Met
                245                 250                 255

Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro
                260                 265                 270

Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln
                275                 280                 285

Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val Gln
    290                 295                 300

Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala
305                 310                 315                 320

Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly Pro
                325                 330                 335

Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln Val Thr Asn
                340                 345                 350
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Thr Ala Thr Ile Met Met Gln Arg Gly Asn Phe Arg Asn Gln Arg Lys
        355                 360                 365

Met Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Thr Ala Arg Asn
        370                 375                 380

Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu Gly
385                 390                 395                 400

His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly Lys
                405                 410                 415

Ile Trp Pro Ser Tyr Lys Gly Arg Pro Gly Asn Phe Leu Gln Ser Arg
            420                 425                 430

Pro Glu Pro Thr Ala Pro Pro Phe Leu Gln Ser Arg Pro Glu Pro Thr
        435                 440                 445

Ala Pro Pro Glu Glu Ser Phe Arg Ser Gly Val Glu Thr Thr Thr Pro
    450                 455                 460

Pro Gln Lys Gln Glu Pro Ile Asp Lys Glu Leu Tyr Pro Leu Thr Ser
465                 470                 475                 480

Leu Arg Ser Leu Phe Gly Asn Asp Pro Ser Ser Gln
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<210>  19
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<212>  DNA
<213>  Artificial sequence

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<223>  Modified Env from HIV strain pNL4-3

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aagcatccag gaagtcagcc taaaactgct tgtaccaatt gctattgtaa aaagtgttgc     180

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cagtaagtag tacatgtaat gcaacctata atagtagcaa tagtagcatt agtagtagca     360

ataataatag caatagttgt gtggtccata gtaatcatag aatataggaa aatattaaga     420

caaagaaaaa tagacaggtt aattgataga ctaatagaaa gagcagaaga cagtggcaat     480
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gttgcaactc acagtctggg gcatcaaaca gctccaggca agaatcctgg ctgtggaaag   2220

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aattgaagaa tcgcaaaacc agcaagaaaa gaatgaacaa gaattattgg aattagataa   2460

atgggcaagt ttgtggaatt ggtttaacat aacaaattgg ctgtggtata taaaattatt   2520

cataatgata gtaggaggct tggtaggttt aagaatagtt tttgctgtac tttctatagt   2580

gaatagagtt aggcagggat attcaccatt atcgtttcag acccacctcc caatcccgag   2640

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<213>  Artificial sequence

<220>
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aagcatccag gaagtcagcc taaaactgct tgtaccaatt gctattgtaa aaagtgttgc   180

tttcattgcc aagtttgttt catgacaaaa gccttaggca tctcctatgg caggaagaag   240

cggagacagc gacgaagagc tcatcagaac agtcagactc atcaagcttc tctatcaaag   300

cagtaagtag tacatgtaat gcaacctata atagtagcaa tagtagcatt agtagtagca   360

ataataatag caatagttgt gtggtccata gtaatcatag aatataggaa aatattaaga   420

caaagaaaaa tagacaggtt aattgataga ctaatagaaa gagcagaaga cagtggcaat   480

gagagtgaag gagaagtatc agcacttgtg gagatggggg tggaaatggg gcaccatgct   540

ccttgggata ttgatgatct gtagtgctac agaaaaattg tgggtcacag tctattatgg   600

ggtacctgtg tggaaggaag caaccaccac tctattttgt gcatcagatg ctaaagcata   660

tgatacagag gtacataatg tttgggccac acatgcctgt gtacccacag accccaaccc   720

acaagaagta gtattggtaa atgtgacaga aaattttaac atgtggaaaa atgacatggt   780

agaacagatg catgaggata taatcagttt atgggatcaa agcctaaagc catgtgtaaa   840
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taataataag acgttcaatg gaacaggacc atgtacaaat gtcagcacag tacaatgtac   1020

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agatgtagta attagatctg ccaatttcac agacaatgct aaaaccataa tagtacagct   1140

gaacacatct gtagaaatta attgtacaag acccaacaac aatacaagaa aaagtatccg   1200

tatccagagg ggaccaggga gagcatttgt tacaatagga aaaataggaa atatgagaca   1260

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attaagagaa caatttggaa ataataaaac aataatcttt aagcaatcct caggagggga   1380

cccagaaatt gtaacgcaca gtttttaattg tggaggggaa ttttctact gtaattcaac   1440

acaactgttt aatagtactt ggtttaatag tacttggagt actgaagggt caaataacac   1500

tgaaggaagt gacacaatca cactcccatg cagaataaaa caatttataa acatgtggca   1560

ggaagtagga aaagcaatgt atgcccctcc catcagtgga caaattagat gttcatcaaa   1620

tattactggg ctgctattaa caagagatgg tggtaataac aacaatgggt ccgagatctt   1680

cagacctgga ggaggcgata tgagggacaa ttggagaagt gaattatata aatataaagt   1740

agtaaaaatt gaaccattag gagtagcacc caccaaggca agagaagag tggtgcagac   1800

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gcagcagaac aatttgctga gggctattga ggcgcaacag catctgttgc aactcacagt   1980

ctggggcatc aaacagctcc aggcaagaat cctggctgtg gaaagatacc taaaggatca   2040

acagctcctg gggatttggg gttgctctgg aaaactcatt tgcaccactg ctgtgccttg   2100

gaatgctagt tggagtaata aatctctgga acagatttgg aataacatga cctggatgga   2160

gtgggacaga gaaattaaca attacacaag cttaatacac tccttaattg aagaatcgca   2220

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gaattggttt aacataacaa attggctgtg gtatataaaa ttattcataa tgatagtagg   2340

aggcttggta ggtttaagaa tagttttttgc tgtactttct atagtgaata gagttaggca   2400

gggatattca ccattatcgt ttcagaccca cctcccaatc ccgaggggac ccgacaggcc   2460

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cggatcctta gcacttatct gggacgatct gcggagcctg tgcctcttca gctaccaccg   2580

cttgagagac ttactcttga ttgtaacgag gattgtggaa cttctgggac gcagggggtg   2640
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ggaagccctc aaatattggt ggaatctcct acagtattgg agtcaggaac taaagaatag          2700

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gaagcatcca ggaagtcagc ctaaaactgc ttgtaccaat tgctattgta aaaagtgttg         180

ctttcattgc caagtttgtt tcataacaaa agccttaggc atctcctatg caggaagaa          240

gcggagacag cgacgaagac ctcctcaagg cagtcagact catcaagttt ctctatcaaa         300

gcagtaagta gtacatgtaa tgcaacctat acaaatagca atagtagcat tagtagtagc         360

aataataata gcaatagttg tgtggtccat agtaatcata gaatatagga aatattaag          420

acaaagaaaa atagacaggt taattgatag actaatagaa agagcagaag acagtggcaa         480

tgagagtgaa ggagaaatat cagcacttgt ggagatgggg gtggagatgg gcaccatgc          540

tccttgggat gttgatgatc tgtagtgcta cagaaaaatt gtgggtcaca gtctattatg         600

gggtacctgt gtggaaggaa gcaaccacca ctctattttg tgcatcagat gctaaagcat         660

atgatacaga ggtacataat gtttgggcca cacatgcctg tgtacccaca gaccccaacc         720

cacaagaagt agtattggta aatgtgacag aaaattttaa catgtggaaa aatgacatgg         780

tagaacagat gcatgaggat ataatcagtt tatgggatca aagcctaaag ccatgtgtaa         840

aattaacccc actctgtgtt agtttaaagt gcactgattt gaagaatgat actaatacca         900

atagtagtag cgggagaatg ataatggaga aaggagagat aaaaaactgc tctttcaata         960

tcagcacaag cataagaggt aaggtgcaga agaatatgc atttttttat aaacttgata        1020

taataccaat agataatgat actaccagct atacgttgac aagttgtaac acctcagtca       1080

ttacacaggc ctgtccaaag gtatcctttg agccaattcc catacattat tgtgccccgg       1140

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ctaaaaccat aatagtacag ctgaaccaat ctgtagaaat taattgtaca agacccaaca       1380

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gacaaattag atgttcatca aatattacag ggctgctatt aacaagagat ggtggtaata    1860

gcaacaatga gtccgagatc ttcagacctg gaggaggaga tatgagggac aattggagaa    1920

gtgaattata taaatataaa gtagtaaaaa ttgaaccatt aggagtagca cccaccaagg    1980

caaagagaag agtggtgcag actagtgcag tgggaatagg agctttgttc cttgggttct    2040

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<213>  Artificial sequence

<220>
<223>  Modified Env/Nef from strain BH10

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acagtctatt atggggtacc tgtgtggaag gaagcaacca ccactctatt ttgtgcatca       180

gatgctaaag catatgatac agaggtacat aatgtttggg ccacacatgc ctgtgtaccc       240

acagacccca acccacaaga agtagtattg gtaaatgtga cagaaaattt taacatgtgg       300

aaaaatgaca tggtagaaca gatgcatgag gatataatca gtttatggga tcaaagccta       360

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tgctctttca atatcagcac aagcataaga ggtaaggtgc agaaagaata tgcatttttt       540

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ggaccatgta caaatgtcag cacagtacaa tgtacacatg gaattaggcc agtagtatca       780

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tttgttacaa taggaaaaat aggaaatatg agacaagcac attgtaacat tagtagagca      1020

aaatggaata acactttaaa acagatagat agcaaattaa gagaacaatt tggaaataat      1080

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aatagtactt ggagtactaa agggtcaaat aacactgaag gaagtgacac aatcaccctc      1260

ccatgcagaa taaaacaaat tataaacatg tggcaggaag taggaaaagc aatgtatgcc      1320

cctcccatca gtggacaaat tagatgttca tcaaatatta cagggctgct attaacaaga      1380
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ctggaacaga tttggaataa catgacctgg atggagtggg acagagaaat taacaattac    1920

acaagcttaa tacactcctt aattgaagaa tcgcaaaacc agcaagaaaa gaatgaacaa    1980

gaattattgg aattagataa atgggcaagt ttgtggaatt ggtttaacat aacaaattgg    2040

ctgtggtata taaaattatt cataatgata gtaggaggct tggtaggttt aagaatagtt    2100

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acgaggattg tggaacttct gggacgcagg gggtgggaag ccctcaaata ttggtggaat    2400

ctcctacagt attggagtca ggagctaaag aatagtgctg ttagcttgct caatgccaca    2460

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gggtggcaag tggtcaaaaa gtagtgtggt tggatggcct gctgtaaggg aaagaatgag    2640

acgagctgag ccagcagcag atggggtggg agcagcatct cgagacctag aaaaacatgg    2700

agcaatcaca agtagcaaca cagcagctaa caatgctgat tgtgcctggc tagaagcaca    2760

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caaggcagct gtagatctta gccacttttt aaaagaaaag gggggactgg aagggctaat    2880

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<210>    23
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<212>    DNA
<213>    Artificial sequence

<220>
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ctttcattgc caagtttgtt tcataacaaa agccttaggc atctcctatg gcaggaagaa     240

gcggagacag cgacgaagac ctcctcaagg cagtcagact catcaagttt ctctatcaaa     300

gcagtaagta gtacatgtaa tgcaacctat acaaatagca atagtagcat tagtagtagc     360

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acaaagaaaa atagacaggt taattgatag actaatagaa agagcagaag acagtggcaa     480

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aattattcat aatgatagta ggaggcttgg taggtttaag aatagttttt gctgtacttt    2580

ctgtagtgaa tagagttagg cagggatatt caccattatc gtttcagacc cacctcccaa    2640

tcccgagggg acccgacagg cccgaaggaa tagaagaaga aggtggagag agagacagag    2700

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<210> 24
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<213> Artificial sequence

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gatgctaaag catatgatac agaggtacat aatgtttggg ccacacatgc ctgtgtaccc    240

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tattgtgccc cggctggttt tgcgattcta aaatgtaata ataagacgtt caatggaaca    720

ggaccatgta caaatgtcag cacagtacaa tgtacacatg gaattaggcc agtagtatca    780

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acaagaccca acaacaatac aagaaaaagt atccgtatcc agagaggacc agggagagca    960

tttgttacaa taggaaaaat aggaaatatg agacaagcac attgtaacat tagtagagca   1020

aaatggaata cactttaaa acagatagat agcaaattaa gagaacaatt tggaaataat   1080

aaaacaataa tctttaagca gtcctcagga ggggacccag aaaattgtaac gcacagtttt   1140

aattgtggag gggaattttt ctactgtaat tcaacacaac tgtttaatag tacttggtttt   1200

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ccatgcagaa taaaacaaat tataaacatg tggcaggaag taggaaaagc aatgtatgcc   1320

cctcccatca gtggacaaat tagatgttca tcaaatatta cagggctgct attaacaaga   1380

gatggtggta atagcaacaa tgagtccgag atcttcagac ctggaggagg agatatgagg   1440

gacaattgga gaagtgaatt atataaatat aaagtagtaa aaattgaacc attaggagta   1500

gcacccacca aggcaaagag aagagtggtg cagagagaaa aaagagcagt gggaatagga   1560

gctttgttcc ttgggttctt gggagcagca ggaagcacta tgggcgcagc gtcaatgacg   1620

ctgacggtac aggccagaca attattgtct ggtatagtgc agcagcagaa caatttgctg   1680

agggctattg aggcgcaaca gcatctgttg caactcacag tctggggcat caagcagctc   1740

caggcaagaa tcctggctgt ggaaagatac ctaaaggatc aacagctcct ggggatttgg   1800

ggttgctctg gaaaactcat ttgcaccact gctgtgcctt ggaatgctag ttggagtaat   1860

aaatctctgg aacagatttg gaataacatg acctggatgg agtgggacag agaaattaac   1920

aattacacaa gcttaataca ctccttaatt gaagaatcgc aaaaccagca agaaaagaat   1980

gaacaagaat tattggaatt agataaatgg gcaagtttgt ggaattggtt taacataaca   2040

aattggctgt ggtatataaa attattcata atgatagtag gaggcttggt aggtttaaga   2100

atagttttttg ctgtactttc tgtagtgaat agagttaggc agggatattc accattatcg   2160

tttcagaccc acctcccaat cccgagggga cccgacaggc ccgaaggaat agaagaagaa   2220

ggtggagaga gagacagaga cagatccatt cgattagtga cggatccttt agcacttatc   2280

tgggacgatc tgcggagcct gtgcctcttc agctaccacc gcttgagaga cttactcttg   2340
```

```
attgtaacga ggattgtgga acttctggga cgcagggggt gggaagccct caaatattgg    2400

tggaatctcc tacagtattg gagtcaggag ctaaagaata gtgctgttag cttgctcaat    2460

gccacagcta tagcagtagc tgaggggaca gatagggtta tagaagtagt acaaggagct    2520

tatagagcta ttcgccacat acctagaaga ataagacagg gcttggaaag gatttttgcta   2580

taa                                                                  2583


<210>   25
<211>   108
<212>   DNA
<213>   Human immunodeficiency virus type 1

<400>   25
tgtacaagac ccaacaacaa tacaagaaaa agtatccgta tccagagagg accagggaga      60

gcatttgtta caataggaaa aataggaaat atgagacaag cacattgt                  108


<210>   26
<211>   105
<212>   DNA
<213>   Human immunodeficiency virus type 1

<400>   26
tgtaccagac ctaacaacaa tacaagaaaa agtgtacgta taggaccagg acaaacattc      60

tatgcaacag gtgatataat aggggatata agacaagcac attgt                     105


<210>   27
<211>   105
<212>   DNA
<213>   Human immunodeficiency virus type 1

<400>   27
tgtacgagac ccaacaataa tacaagaaaa agtataagga taggaccagg acaagcattc      60

tatgcaacag gagaaataat aggagatata agacaagcac attgt                     105


<210>   28
<211>   102
<212>   DNA
<213>   Human immunodeficiency virus type 1

<400>   28
tgcacaaggc cctacaacaa tataagacaa aggaccccca taggactagg gcaagcactc      60

tatacaacaa gaagaataga agatataaga agagcacatt gt                        102


<210>   29
<211>   105
<212>   DNA
<213>   Human immunodeficiency virus type 1
```

<400> 29
tgtaccagac cctccaccaa tacaagaaca agtatacgta taggaccagg acaagtattc     60

tatagaacag gagacataac aggagatata agaaaagcat attgt                    105


<210> 30
<211> 105
<212> DNA
<213> Human immunodeficiency virus type 1

<400> 30
tgtacaagac ccaacaacaa tacaagaaaa agaatatctt taggaccagg acgagtattt     60

tatacagcag gagaaataat aggagacatc agaaaggcac attgt                    105


<210> 31
<211> 105
<212> DNA
<213> Human immunodeficiency virus type 1

<400> 31
tgtaccagac ctaataacaa tacaagaaaa agtataactt ttgcaccagg acaagcgctc     60

tatgcaacag gtgaaataat aggagatata agacaagcac attgt                    105


<210> 32
<211> 2562
<212> DNA
<213> Artificial sequence

<220>
<223> Env with multi-clade V3 loops

<400> 32
atgagagtga aggagaaata tcagcacttg tggagatggg ggtggagatg gggcaccatg     60

ctccttggga tgttgatgat ctgtagtgct acagaaaaat gtgggtcac  agtctattat    120

ggggtacctg tgtggaagga agcaaccacc actctatttt gtgcatcaga tgctaaagca    180

tatgatacag aggtacataa tgtttgggcc acacatgcct gtgtacccac agaccccaac    240

ccacaagaag tagtattggt aaatgtgaca gaaaatttta acatgtggaa aaatgacatg    300

gtagaacaga tgcatgagga tataatcagt ttatgggatc aaagcctaaa gccatgtgta    360

aaattaaccc cactctgtgt tggagctggt agttgtaaca cctcagtcat tacacaggcc    420

tgtccaaagg tatcctttga gccaattccc atacattatt gtgccccggc tggttttgcg    480

attctaaaat gtaataataa gacgttcaat ggaacaggac catgtacaaa tgtcagcaca    540

gtacaatgta cacatggaat taggccagta gtatcaactc aactgctgtt aaatggcagt    600

ctggcagaag aagaggtagt aattagatct gccaatttca cagacaatgc taaaaccata    660

atagtacagc tgaaccaatc tgtagaaatt aattgtacaa gacccaacaa caatacaaga    720

```
aaaagtatcc gtatccagag aggaccaggg agagcatttg ttacaatagg aaaaatagga    780

aatatgagac aagcacattg tctcgggtgt accagaccta acaacaatac aagaaaaagt    840

gtacgtatag gaccaggaca aacattctat gcaacaggtg atataatagg ggatataaga    900

caagcacatt gttgtacgag acccaacaat aatacaagaa aaagtataag gataggacca    960

ggacaagcat tctatgcaac aggagaaata ataggagata taagacaagc acattgttgc   1020

acaaggccct acaacaatat aagacaaagg acccccatag gactagggca agcactctat   1080

acaacaagaa gaatagaaga tataagaaga gcacattgtt gtaccagacc ctccaccaat   1140

acaagaacaa gtatacgtat aggaccagga caagtattct atagaacagg agacataaca   1200

ggagatataa gaaaagcata ttgtggatcc tgtacaagac ccaacaacaa tacaagaaaa   1260

agaatatctt taggaccagg acgagtattt tatacagcag gagaaataat aggagacatc   1320

agaaaggcac attgttgtac cagacctaat aacaatacaa gaaaaagtat aacttttgca   1380

ccaggacaag cgctctatgc aacaggtgaa ataataggag atataagaca agcacattgt   1440

ctcgggaaca ttagtagagc aaaatggaat aacactttaa acagataga tagcaaatta    1500

agagaacaat ttggaaataa taaaacaata atctttaagc agtcctcagg aggggaccca   1560

gaaattgtaa cgcacagttt taattgtgga ggggaatttt tctactgtaa ttcaacacaa   1620

ctgtttaata gtacttggtt taatagtact tggagtacta aagggtcaaa taacactgaa   1680

ggaagtgaca caatcaccct cccatgcaga ataaaacaaa ttataaacat gtggcaggaa   1740

gtaggaaaag caatgtatgc ccctcccatc agtggacaaa ttagatgttc atcaaatatt   1800

acagggctgc tattaacaag agatggtggt aatagcaaca atgagtccga gatcttcaga   1860

cctggaggag gagatatgag ggacaattgg agaagtgaat tatataaata taaagtagta   1920

aaaattgaac cattaggagt agcacccacc aaggcaaaga gaagagtggt gcagactagt   1980

gcagtgggaa taggagcttt gttccttggg ttcttgggag cagcaggaag cactatgggc   2040

gcagcgtcaa tgacgctgac ggtacaggcc agacaattat tgtctggtat agtgcagcag   2100

cagaacaatt tgctgagggc tattgaggcg caacagcatc tgttgcaact cacagtctgg   2160

ggcatcaagc agctccaggc aagaatcctg gctgtggaaa gatacctaaa ggatcaacag   2220

ctcctgggga tttggggttg ctctggaaaa ctcatttgca ccactgctgt gccttggaat   2280

gctagttgga gtaataaatc tctggaacag atttggaata acatgacctg gatggagtgg   2340

gacagagaaa ttaacaatta cacaagctta atacactcct taattgaaga atcgcaaaac   2400

cagcaagaaa agaatgaaca agaattattg gaattagata atgggcaag tttgtggaat    2460

tggtttaaca taacaaattg gctgtggtat ataaaatcgt ggctgctgct gctcctgctc   2520

tccctctccc tcctccaggc cacggatttc atgtccctgt ga                     2562
```

<210> 33
<211> 853
<212> PRT
<213> Artificial sequence

<220>
<223> Modified Env with multi-clade V3 loops

<400> 33

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1               5                   10                  15


Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
                20                  25                  30


Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
            35                  40                  45


Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
        50                  55                  60


Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80


Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95


Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
                100                 105                 110


Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Gly
        115                 120                 125


Ala Gly Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
        130                 135                 140


Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
145                 150                 155                 160


Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
                165                 170                 175


Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
            180                 185                 190


Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
    210                 215                 220

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
225                 230                 235                 240

Lys Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile
            245                 250                 255

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Leu Gly Cys Thr Arg
        260                 265                 270

Pro Asn Asn Asn Thr Arg Lys Ser Val Arg Ile Gly Pro Gly Gln Thr
        275                 280                 285

Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys
        290                 295                 300

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Arg Ile Gly Pro
305                 310                 315                 320

Gly Gln Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln
            325                 330                 335

Ala His Cys Cys Thr Arg Pro Tyr Asn Asn Ile Arg Gln Arg Thr Pro
            340                 345                 350

Ile Gly Leu Gly Gln Ala Leu Tyr Thr Thr Arg Arg Ile Glu Asp Ile
        355                 360                 365

Arg Arg Ala His Cys Cys Thr Arg Pro Ser Thr Asn Thr Arg Thr Ser
    370                 375                 380

Ile Arg Ile Gly Pro Gly Gln Val Phe Tyr Arg Thr Gly Asp Ile Thr
385                 390                 395                 400

Gly Asp Ile Arg Lys Ala Tyr Cys Gly Ser Cys Thr Arg Pro Asn Asn
            405                 410                 415

Asn Thr Arg Lys Arg Ile Ser Leu Gly Pro Gly Arg Val Phe Tyr Thr
        420                 425                 430

Ala Gly Glu Ile Ile Gly Asp Ile Arg Lys Ala His Cys Cys Thr Arg
        435                 440                 445

```
Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Phe Ala Pro Gly Gln Ala
    450                 455                 460

Leu Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys
465                 470                 475                 480

Leu Gly Asn Ile Ser Arg Ala Lys Trp Asn Asn Thr Leu Lys Gln Ile
                485                 490                 495

Asp Ser Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe
                500                 505                 510

Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn
            515                 520                 525

Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser
    530                 535                 540

Thr Trp Phe Asn Ser Thr Trp Ser Thr Lys Gly Ser Asn Asn Thr Glu
545                 550                 555                 560

Gly Ser Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn
                565                 570                 575

Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly
            580                 585                 590

Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp
        595                 600                 605

Gly Gly Asn Ser Asn Asn Glu Ser Glu Ile Phe Arg Pro Gly Gly Gly
    610                 615                 620

Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val
625                 630                 635                 640

Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val
                645                 650                 655

Val Gln Thr Ser Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
            660                 665                 670

Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val
            675                 680                 685
```

```
Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
    690                 695                 700
```

```
Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
705                 710                 715                 720
```

```
Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr Leu
                725                 730                 735
```

```
Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
                740                 745                 750
```

```
Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
                755                 760                 765
```

```
Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
    770                 775                 780
```

```
Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
785                 790                 795                 800
```

```
Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
                805                 810                 815
```

```
Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
                820                 825                 830
```

```
Ser Trp Leu Leu Leu Leu Leu Leu Ser Leu Ser Leu Leu Gln Ala Thr
                835                 840                 845
```

```
Asp Phe Met Ser Leu
    850
```

```
<210>   34
<211>   1092
<212>   DNA
<213>   Human immunodeficiency virus type 1
```

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<400>   34
atgggtgcga gagcgtcagt attaagcggg ggagaattag atcgatggga aaaaattcgg    60

ttaaggccag ggggaaagaa aaaatataaa ttaaaacata tagtatgggc aagcagggag   120

ctagaacgat tcgcagttaa tcctggcctg ttagaaacat cagaaggctg tagacaaata   180

ctgggacagc tacaaccatc ccttcagaca ggatcagaag aacttagatc attatataat   240

acagtagcaa ccctctattg tgtgcatcaa aggatagaga taaaagacac caaggaagct   300
```

```
ttagacaaga tagaggaaga gcaaaacaaa agtaagaaaa aagcacagca agcagcagct       360

gacacaggac acagcagtca ggtcagccaa aattacccta tagtgcagaa catccagggg       420

caaatggtac atcaggccat atcacctaga actttaaatg catgggtaaa agtagtagaa       480

gagaaggctt tcagcccaga agtaataccc atgttttcag cattatcaga aggagccacc       540

ccacaagatt taaacaccat gctaaacaca gtggggggac atcaagcagc catgcaaatg       600

ttaaaagaga ccatcaatga ggaagctgca gaatgggata gagtacatcc agtgcatgca       660

gggcctattg caccaggcca gatgagagaa ccaaggggaa gtgacatagc aggaactact       720

agtacccttc aggaacaaat aggatggatg acaaataatc cacctatccc agtaggagaa       780

atttataaaa gatggataat cctgggatta aataaaatag taagaatgta tagccctacc       840

agcattctgg acataagaca aggaccaaaa gaacctttta gagactatgt agaccggttc       900

tataaaactc taagagccga gcaagcttca caggaggtaa aaaattggat gacagaaacc       960

ttgttggtcc aaaatgcgaa cccagattgt aagactattt taaaagcatt gggaccagcg      1020

gctacactag aagaaatgat gacagcatgt cagggagtag gaggacccgg ccataaggca      1080

agagttttgt aa                                                           1092


<210>   35
<211>   1179
<212>   DNA
<213>   Human immunodeficiency virus type 1

<400>   35
atgagagtga aggagaaata tcagcacttg tggagatggg ggtggagatg gggcaccatg        60

ctccttggga tgttgatgat ctgtagtgct ggtgcgagag cgtcagtatt aagcggggga       120

gaattagatc gatgggaaaa aattcggtta aggccagggg gaaagaaaaa atataaatta       180

aaacatatag tatgggcaag cagggagcta gaacgattcg cagttaatcc tggcctgtta       240

gaaacatcag aaggctgtag acaaatactg ggacagctac aaccatccct tcagacagga       300

tcagaagaac ttagatcatt atataataca gtagcaaccc tctattgtgt gcatcaaagg       360

atagagataa aagacaccaa ggaagcttta gacaagatag gaagagcaa aaacaaaagt       420

aagaaaaaag cacagcaagc agcagctgac acaggacaca gcagtcaggt cagccaaaat       480

taccctatag tgcagaacat ccaggggcaa atggtacatc aggccatatc acctagaact       540

ttaaatgcat gggtaaaagt agtagaagag aaggctttca gcccagaagt aatacccatg       600

ttttcagcat tatcagaagg agccacccca caagatttaa acaccatgct aaacacagtg       660

gggggacatc aagcagccat gcaaatgtta aaagagacca tcaatgagga agctgcagaa       720

tgggatagag tacatccagt gcatgcaggg cctattgcac caggccagat gagagaacca       780
```

```
agggggaagtg acatagcagg aactactagt acccttcagg aacaaatagg atggatgaca      840

aataatccac ctatcccagt aggagaaatt tataaaagat ggataatcct gggattaaat      900

aaaatagtaa gaatgtatag ccctaccagc attctggaca taagacaagg accaaaagaa      960

ccttttagag actatgtaga ccggttctat aaaactctaa gagccgagca agcttcacag     1020

gaggtaaaaa attggatgac agaaaccttg ttggtccaaa atgcgaaccc agattgtaag     1080

actattttaa aagcattggg accagcggct acactagaag aaatgatgac agcatgtcag     1140

ggagtaggag gacccggcca taaggcaaga gttttgtaa                            1179


<210>   36
<211>   1308
<212>   DNA
<213>   Human immunodeficiency virus type 1

<400>   36
atgagagtga aggagaaata tcagcacttg tggagatggg ggtggagatg gggcaccatg       60

ctccttggga tgttgatgat ctgtagtgct ggtgcgagag cgtcagtatt aagcggggga      120

gaattagatc gatgggaaaa aattcggtta aggccagggg gaaagaaaaa atataaatta      180

aaacatatag tatgggcaag cagggagcta gaacgattcg cagttaatcc tggcctgtta      240

gaaacatcag aaggctgtag acaaatactg ggacagctac aaccatccct tcagacagga      300

tcagaagaac ttagatcatt atataataca gtagcaaccc tctattgtgt gcatcaaagg      360

atagagataa aagacaccaa ggaagcttta gacaagatag aggaagagca aaacaaaagt      420

aagaaaaag cacagcaagc agcagctgac acaggacaca gcagtcaggt cagccaaaat      480

taccctatag tgcagaacat ccagggggcaa atggtacatc aggccatatc acctagaact      540

ttaaatgcat gggtaaaagt agtagaagag aaggctttca gcccagaagt aatacccatg      600

ttttcagcat tatcagaagg agccacccca caagatttaa acaccatgct aaacacagtg      660

ggggggacatc aagcagccat gcaaatgtta aaagagacca tcaatgagga agctgcagaa      720

tgggatagag tacatccagt gcatgcaggg cctattgcac caggccagat gagagaacca      780

agggggaagtg acatagcagg aactactagt acccttcagg aacaaatagg atggatgaca      840

aataatccac ctatcccagt aggagaaatt tataaaagat ggataatcct gggattaaat      900

aaaatagtaa gaatgtatag ccctaccagc attctggaca taagacaagg accaaaagaa      960

ccttttagag actatgtaga ccggttctat aaaactctaa gagccgagca agcttcacag     1020

gaggtaaaaa attggatgac agaaaccttg ttggtccaaa atgcgaaccc agattgtaag     1080

actattttaa aagcattggg accagcggct acactagaag aaatgatgac agcatgtcag     1140

ggagtaggag gacccggcca taaggcaaga gttttgttat tcataatgat agtaggaggc     1200
```

ttggtaggtt taagaatagt ttttgctgta ctttctgtag tgaatagagt taggcaggga    1260

tattcaccat tatcgtttca gacccacctc ccaatcccga ggggataa    1308


<210> 37
<211> 363
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 37

Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp
1               5                   10                  15

Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
            20                  25                  30

His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
        35                  40                  45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
    50                  55                  60

Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
65                  70                  75                  80

Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
                85                  90                  95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
            100                 105                 110

Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val
        115                 120                 125

Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His
    130                 135                 140

Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
145                 150                 155                 160

Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser
                165                 170                 175

Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly
            180                 185                 190

Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu

Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala
    210                 215                 220

Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr
225                 230                 235                 240

Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile
                245                 250                 255

Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys
                260                 265                 270

Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly
        275                 280                 285

Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
    290                 295                 300

Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr
305                 310                 315                 320

Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala
                325                 330                 335

Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly
            340                 345                 350

Val Gly Gly Pro Gly His Lys Ala Arg Val Leu
        355                 360


<210>  38
<211>  410
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  38

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Gly Ala
            20                  25                  30

Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp Glu Lys Ile
        35                  40                  45

Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys His Ile Val
    50              55              60

Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro Gly Leu Leu
65              70              75              80

Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu Gln Pro Ser
            85              90              95

Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn Thr Val Ala
            100             105             110

Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp Thr Lys Glu
        115             120             125

Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys Lys Lys Ala
    130             135             140

Gln Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val Ser Gln Asn
145             150             155             160

Tyr Pro Gln Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val Ser
            165             170             175

Gln Asn Tyr Pro Gln Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln
            180             185             190

Val Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val
        195             200             205

His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val
    210             215             220

Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu
225             230             235             240

Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val
            245             250             255

Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu
            260             265             270

Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile
        275             280             285

```
Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr
    290                 295                 300

Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro
305                 310                 315                 320

Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn
                325                 330                 335

Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln
                340                 345                 350

Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr
            355                 360                 365

Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Thr Ile Leu Lys Ala Leu
    370                 375                 380

Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val
385                 390                 395                 400

Gly Gly Pro Gly His Lys Ala Arg Val Leu
                405                 410


<210>  39
<211>  453
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  39

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Gly Ala
            20                  25                  30

Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp Glu Lys Ile
            35                  40                  45

Arg Leu Arg Pro Gly Gly Leu Ser Gly Gly Glu Leu Asp Arg Trp Glu
    50                  55                  60

Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys His
65                  70                  75                  80

Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro Gly
                85                  90                  95
```

```
Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu Gln
        100                 105             110

Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn Thr
        115                 120             125

Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp Thr
        130                 135             140

Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys Lys
145                 150             155                 160

Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val Ser
                165             170                 175

Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His Gln
                180             185             190

Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu
            195             200             205

Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu
    210             215             220

Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly
225             230             235                 240

His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala
            245             250             255

Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro
            260             265             270

Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser
        275             280             285

Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro
    290             295             300

Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile
305             310             315                 320

Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro
            325             330             335
```

```
Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg
            340                 345                 350

Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu
            355                 360                 365

Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu
    370                 375                 380

Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val
385                 390                 395                 400

Gly Gly Pro Gly His Lys Ala Arg Val Leu Leu Phe Ile Met Ile Val
            405                 410                 415

Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val Val
            420                 425                 430

Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His Leu
    435                 440                 445

Pro Ile Pro Arg Gly
    450


<210>  40
<211>  399
<212>  DNA
<213>  Human immunodeficiency virus type 1

<400>  40
atgggtgcga gagcgtcagt attaagcggg ggagaattag atcgatggga aaaaattcgg          60

ttaaggccag ggggaaagaa aaaatataaa ttaaaacata tagtatgggc aagcagggag         120

ctagaacgat tcgcagttaa tcctggcctg ttagaaacat cagaaggctg tagacaaata         180

ctgggacagc tacaaccatc ccttcagaca ggatcagaag aacttagatc attatataat         240

acagtagcaa ccctctattg tgtgcatcaa aggatagaga taaaagacac caaggaagct         300

ttagacaaga tagaggaaga gcaaaacaaa agtaagaaaa agcacagca agcagcagct          360

gacacaggac acagcagtca ggtcagccaa aattactaa                                399


<210>  41
<211>  486
<212>  DNA
<213>  Human immunodeficiency virus type 1

<400>  41
atgagagtga aggagaaata tcagcacttg tggagatggg ggtggagatg gggcaccatg          60
```

```
ctccttggga tgttgatgat ctgtagtgct ggtgcgagag cgtcagtatt aagcggggga    120

gaattagatc gatgggaaaa aattcggtta aggccagggg gaaagaaaaa atataaatta    180

aaacatatag tatgggcaag cagggagcta gaacgattcg cagttaatcc tggcctgtta    240

gaaacatcag aaggctgtag acaaatactg ggacagctac aaccatccct tcagacagga    300

tcagaagaac ttagatcatt atataataca gtagcaaccc tctattgtgt gcatcaaagg    360

atagagataa aagacaccaa ggaagcttta gacaagatag aggaagagca aaacaaaagt    420

aagaaaaaag cacagcaagc agcagctgac acaggacaca gcagtcaggt cagccaaaat    480
                                                                      486
tactaa
```

```
<210>    42
<211>    615
<212>    DNA
<213>    Human immunodeficiency virus type 1

<400>    42
atgagagtga aggagaaata tcagcacttg tggagatggg ggtggagatg gggcaccatg     60

ctccttggga tgttgatgat ctgtagtgct ggtgcgagag cgtcagtatt aagcggggga    120

gaattagatc gatgggaaaa aattcggtta aggccagggg gaaagaaaaa atataaatta    180

aaacatatag tatgggcaag cagggagcta gaacgattcg cagttaatcc tggcctgtta    240

gaaacatcag aaggctgtag acaaatactg ggacagctac aaccatccct tcagacagga    300

tcagaagaac ttagatcatt atataataca gtagcaaccc tctattgtgt gcatcaaagg    360

atagagataa aagacaccaa ggaagcttta gacaagatag aggaagagca aaacaaaagt    420

aagaaaaaag cacagcaagc agcagctgac acaggacaca gcagtcaggt cagccaaaat    480

tacttattca taatgatagt aggaggcttg gtaggtttaa gaatagtttt tgctgtactt    540

tctgtagtga atagagttag gcagggatat tcaccattat cgtttcagac ccacctccca    600
                                                                      615
atcccgaggg gataa
```

```
<210>    43
<211>    132
<212>    PRT
<213>    Human immunodeficiency virus type 1

<400>    43

Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp
1               5                   10                  15


Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
                20                  25                  30
```

His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
    35                     40                  45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
    50                     55                  60

Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
65                     70                 75                  80

Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
          85                     90                  95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
          100                   105                110

Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val
          115                   120                125

Ser Gln Asn Tyr
    130

<210> 44
<211> 179
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 44

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1               5                     10                 15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Gly Ala
          20                     25                30

Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp Glu Lys Ile
          35                     40                45

Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys His Ile Val
          50                     55                60

Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro Gly Leu Leu
65                     70                 75                  80

Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu Gln Pro Ser
          85                     90                95

Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Gly Gln Leu Gln

Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn Thr
        115                 120                 125

Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp Thr
        130                 135                 140

Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys Lys
145                 150                 155                 160

Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val Ser
                165                 170                 175

Gln Asn Tyr


<210>   45
<211>   186
<212>   PRT
<213>   Human immunodeficiency virus type 1

<400>   45

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Gly Ala
            20                  25                  30

Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp Glu Lys Ile
        35                  40                  45

Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys His Ile Val
    50                  55                  60

Trp Ala Ser Arg Glu Leu Glu Arg Gly Gln Leu Gln Pro Ser Leu Gln
65                  70                  75                  80

Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn Thr Val Ala Thr Leu
            85                  90                  95

Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp Thr Lys Glu Ala Leu
            100                 105                 110

Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys Lys Lys Ala Gln Gln
        115                 120                 125

```
Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val Ser Gln Asn Tyr Leu
    130                 135                 140


Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala
145                 150                 155                 160


Val Leu Ser Val Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser
                165                 170                 175


Phe Gln Thr His Leu Pro Ile Pro Arg Gly
                180                 185
```

<210> 46
<211> 699
<212> DNA
<213> Human immunodeficiency virus type 1

<400> 46

```
atgcctatag tgcagaacat ccaggggcaa atggtacatc aggccatatc acctagaact    60

ttaaatgcat gggtaaaagt agtagaagag aaggctttca gcccagaagt aatacccatg   120

tttcagcat tatcagaagg agccacccca caagatttaa acaccatgct aaacacagtg    180

gggggacatc aagcagccat gcaaatgtta aaagagacca tcaatgagga agctgcagaa   240

tgggatagag tacatccagt gcatgcaggg cctattgcac caggccagat gagagaacca   300

aggggaagtg acatagcagg aactactagt acccttcagg aacaaatagg atggatgaca   360

aataatccac ctatcccagt aggagaaatt tataaaagat ggataatcct gggattaaat   420

aaaatagtaa gaatgtatag ccctaccagc attctggaca taagacaagg accaaaagaa   480

ccttttagag actatgtaga ccggttctat aaaactctaa gagccgagca agcttcacag   540

gaggtaaaaa attggatgac agaaaccttg ttggtccaaa atgcgaaccc agattgtaag   600

actattttaa aagcattggg accagcggct acactagaag aaatgatgac agcatgtcag   660

ggagtaggag gacccggcca taaggcaaga gttttgtaa                          699
```

<210> 47
<211> 786
<212> DNA
<213> Human immunodeficiency virus type 1

<400> 47

```
atgagagtga aggagaaata tcagcacttg tggagatggg ggtggagatg gggcaccatg    60

ctccttggga tgttgatgat ctgtagtgct cctatagtgc agaacatcca ggggcaaatg   120

gtacatcagg ccatatcacc tagaacttta aatgcatggg taaagtagt agaagagaag     180

gctttcagcc cagaagtaat acccatgttt tcagcattat cagaaggagc caccccacaa   240
```

```
gatttaaaca ccatgctaaa cacagtgggg ggacatcaag cagccatgca aatgttaaaa      300

gagaccatca atgaggaagc tgcagaatgg gatagagtac atccagtgca tgcagggcct      360

attgcaccag gccagatgag agaaccaagg ggaagtgaca tagcaggaac tactagtacc      420

cttcaggaac aaataggatg gatgacaaat aatccaccta tcccagtagg agaaatttat      480

aaaagatgga taatcctggg attaaataaa atagtaagaa tgtatagccc taccagcatt      540

ctggacataa gacaaggacc aaaagaacct tttagagact atgtagaccg gttctataaa      600

actctaagag ccgagcaagc ttcacaggag gtaaaaaatt ggatgacaga accttgttg      660

gtccaaaatg cgaacccaga ttgtaagact attttaaaag cattgggacc agcggctaca      720

ctagaagaaa tgatgacagc atgtcaggga gtaggaggac ccggccataa ggcaagagtt      780

ttgtaa                                                                  786


<210>  48
<211>  915
<212>  DNA
<213>  Human immunodeficiency virus type 1

<400>  48
atgagagtga aggagaaata tcagcacttg tggagatggg ggtggagatg gggcaccatg       60

ctccttggga tgttgatgat ctgtagtgct cctatagtgc agaacatcca ggggcaaatg      120

gtacatcagg ccatatcacc tagaacttta aatgcatggg taaaagtagt agaagagaag      180

gctttcagcc cagaagtaat acccatgttt tcagcattat cagaaggagc cacccacaa      240

gatttaaaca ccatgctaaa cacagtgggg ggacatcaag cagccatgca aatgttaaaa      300

gagaccatca atgaggaagc tgcagaatgg gatagagtac atccagtgca tgcagggcct      360

attgcaccag gccagatgag agaaccaagg ggaagtgaca tagcaggaac tactagtacc      420

cttcaggaac aaataggatg gatgacaaat aatccaccta tcccagtagg agaaatttat      480

aaaagatgga taatcctggg attaaataaa atagtaagaa tgtatagccc taccagcatt      540

ctggacataa gacaaggacc aaaagaacct tttagagact atgtagaccg gttctataaa      600

actctaagag ccgagcaagc ttcacaggag gtaaaaaatt ggatgacaga accttgttg      660

gtccaaaatg cgaacccaga ttgtaagact attttaaaag cattgggacc agcggctaca      720

ctagaagaaa tgatgacagc atgtcaggga gtaggaggac ccggccataa ggcaagagtt      780

ttgttattca taatgatagt aggaggcttg gtaggtttaa gaatagtttt tgctgtactt      840

tctgtagtga atagagttag gcagggatat tcaccattat cgtttcagac ccacctccca      900

atcccgaggg gataa                                                        915
```

<210> 49
<211> 232
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 49

Met Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His Gln Ala Ile
1               5                   10                  15


Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu Lys Ala
            20                  25                  30


Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala
        35                  40                  45


Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln
    50                  55                  60


Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu
65                  70                  75                  80


Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln
            85                  90                  95


Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu
            100                 105                 110


Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly
        115                 120                 125


Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg
    130                 135                 140


Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu
145                 150                 155                 160


Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu
            165                 170                 175


Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val
        180                 185                 190


Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro
        195                 200                 205


Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
    210                 215                 220

```
Pro Gly His Lys Ala Arg Val Leu
225             230


<210>   50
<211>   261
<212>   PRT
<213>   Human immunodeficiency virus type 1

<400>   50

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1               5                   10                  15


Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Pro Ile
            20                  25                  30


Val Gln Asn Ile Gln Gly Gln Met Val His Gln Ala Ile Ser Pro Arg
        35                  40                  45


Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu Lys Ala Phe Ser Pro
    50                  55                  60


Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln
65                  70                  75                  80


Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln Ala Ala Met
                85                  90                  95


Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu Trp Asp Arg
            100                 105                 110


Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln Met Arg Glu
            115                 120                 125


Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln
    130                 135                 140


Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr
145                 150                 155                 160


Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser
                165                 170                 175


Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg
                180                 185                 190
```

Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser
     195                    200                 205

Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn Ala
     210                    215                 220

Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr
225                230                235                240

Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly Pro Gly His
           245               250                255

Lys Ala Arg Val Leu
          260


<210> 51
<211> 286
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 51

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1              5                    10                15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Pro Ile
           20                    25                30

Val Gln Asn Ile Gln Gly Gln Met Val His Gln Ala Ile Ser Pro Arg
          35                    40                45

Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu Lys Ala Phe Ser Pro
     50                    55                60

Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln
65                70                75                80

Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln Ala Ala Met
           85                    90                95

Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Arg Glu Pro Arg
          100                    105                110

Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly
          115                    120                125

Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg
          130                    135                140

```
Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr
145                 150             155                 160

Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr
                165             170             175

Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu
            180             185             190

Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn Ala Asn Pro
            195             200             205

Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu
        210             215             220

Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly Pro Gly His Lys Ala
225                 230             235                 240

Arg Val Leu Leu Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg
                245             250             255

Ile Val Phe Ala Val Leu Ser Val Val Asn Arg Val Arg Gln Gly Tyr
            260             265             270

Ser Pro Leu Ser Phe Gln Thr His Leu Pro Ile Pro Arg Gly
        275             280             285


<210>   52
<211>   3839
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Modified Env/Tat

<400>   52
gaattctgca acaactgctg tttatccatt ttcagaattg ggtgtcgaca tagcagaata      60

ggcgttactc gacagaggag agcaagaaat ggagccagta gatcctagac tagagccctg     120

gaagcatcca ggaagtcagc ctaaaactgc ttgtaccaat tgctattgta aaaagtgttg     180

ctttcattgc caagtttgtt tcataacaaa agccttaggc atctcctatg gcaggaagaa     240

gcggagacag cgacgaagac ctcctcaagg cagtcagact catcaagttt ctctatcaaa     300

gcagtaagta gtacatgtaa tgcaacctat acaaatagca atagtagcat tagtagtagc     360

aataataata gcaatagttg tgtggtccat agtaatcata gaatatagga aaatattaag     420
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acaaagaaaa atagacaggt taattgatag actaatagaa agagcagaag acagtggcaa      480

tgagagtgaa ggagaaatat cagcacttgt ggagatgggg gtggagatgg ggcaccatgc      540

tccttgggat gttgatgatc tgtagtgcta cagaaaaatt gtgggtcaca gtctattatg      600

gggtacctgt gtggaaggaa gcaaccacca ctctattttg tgcatcagat gctaaagcat      660

atgatacaga ggtacataat gtttgggcca cacatgcctg tgtacccaca gaccccaacc      720

cacaagaagt agtattggta aatgtgacag aaaattttaa catgtggaaa aatgacatgg      780

tagaacagat gcatgaggat ataatcagtt tatgggatca aagcctaaag ccatgtgtaa      840

aattaacccc actctgtgtt ggagctggta gttgtaacac ctcagtcatt acacaggcct      900

gtccaaaggt atcctttgag ccaattccca tacattattg tgccccggct ggttttgcga      960

ttctaaaatg taataataag acgttcaatg gaacaggacc atgtacaaat gtcagcacag     1020

tacaatgtac acatggaatt aggccagtag tatcaactca actgctgtta aatggcagtc     1080

tggcagaaga agaggtagta attagatctg ccaatttcac agacaatgct aaaaccataa     1140

tagtacagct gaaccaatct gtagaaatta attgtacaag acccaacaac aatacaagaa     1200

aaagtatccg tatccagaga ggaccaggga gagcatttgt tacaatagga aaaataggaa     1260

atatgagaca agcacattgt ctcgggtgta ccagacctaa caacaataca agaaaaagtg     1320

tacgtatagg accaggacaa acattctatg caacaggtga tataataggg gatataagac     1380

aagcacattg ttgtacgaga cccaacaata atacaagaaa aagtataagg ataggaccag     1440

gacaagcatt ctatgcaaca ggagaaataa taggagatat aagacaagca cattgttgca     1500

caaggcccta caacaatata agacaaagga cccccatagg actagggcaa gcactctata     1560

caacaagaag aatagaagat ataagaagag cacattgttg taccagaccc tccaccaata     1620

caagaacaag tatacgtata ggaccaggac aagtattcta tagaacagga gacataacag     1680

gagatataag aaaagcatat tgtggatcct gtacaagacc caacaacaat acaagaaaaa     1740

gaatatcttt aggaccagga cgagtatttt atacagcagg agaaataata ggagacatca     1800

gaaaggcaca ttgttgtacc agacctaata caatacaag aaaaagtata acttttgcac     1860

caggacaagc gctctatgca acaggtgaaa ataggaga tataagacaa gcacattgtc     1920

tcgggtgtac cagacctaac aacaatacaa gaaaaagtgt acgtatagga ccaggacaaa     1980

cattctatgc aacaggtgat ataatagggg atataagaca agcacattgt tgtacgagac     2040

ccaacaataa tacaagaaaa agtataagga taggaccagg acaagcattc tatgcaacag     2100

gagaaataat aggagatata agacaagcac attgttgcac aaggccctac aacaatataa     2160

gacaaaggac ccccatagga ctagggcaag cactctatac aacaagaaga atagaagata     2220

taagaagagc acattgttgt accagaccct ccaccaatac aagaacaagt atacgtatag     2280
```

gaccaggaca agtattctat agaacaggag acataacagg agatataaga aaagcatatt      2340

gtggatcctg tacaagaccc aacaacaata caagaaaaag aatatcttta ggaccaggac      2400

gagtatttta tacagcagga gaaataatag gagacatcag aaaggcacat tgttgtacca      2460

gacctaataa caatacaaga aaaagtataa cttttgcacc aggacaagcg ctctatgcaa      2520

caggtgaaat aataggagat ataagacaag cacattgtct cgggaacatt agtagagcaa      2580

aatggaataa cactttaaaa cagatagata gcaaattaag agaacaattt ggaaataata      2640

aaacaataat ctttaagcag tcctcaggag gggacccaga aattgtaacg cacagtttta      2700

attgtggagg ggaattttc tactgtaatt caacacaact gtttaatagt acttggttta      2760

atagtacttg gagtactaaa gggtcaaata acactgaagg aagtgacaca atcaccctcc      2820

catgcagaat aaaacaaatt ataaacatgt ggcaggaagt aggaaaagca atgtatgccc      2880

ctcccatcag tggacaaatt agatgttcat caaatattac agggctgcta ttaacaagag      2940

atggtggtaa tagcaacaat gagtccgaga tcttcagacc tggaggagga gatatgaggg      3000

acaattggag aagtgaatta tataaatata agtagtaaa aattgaacca ttaggagtag      3060

cacccaccaa ggcaaagaga agagtggtgc agactagtgc agtgggaata ggagctttgt      3120

tccttgggtt cttgggagca gcaggaagca ctatgggcgc agcgtcaatg acgctgacgg      3180

tacaggccag acaattattg tctggtatag tgcagcagca gaacaatttg ctgagggcta      3240

ttgaggcgca acagcatctg ttgcaactca cagtctgggg catcaagcag ctccaggcaa      3300

gaatcctggc tgtggaaaga tacctaaagg atcaacagct cctggggatt tggggttgct      3360

ctggaaaact catttgcacc actgctgtgc cttggaatgc tagttggagt aataaatctc      3420

tggaacagat ttggaataac atgacctgga tggagtggga cagagaaatt aacaattaca      3480

caagcttaat acactcctta attgaagaat cgcaaaacca gcaagaaaag aatgaacaag      3540

aattattgga attagataaa tgggcaagtt tgtggaattg gtttaacata caaaattggc      3600

tgtggtatat aaaattattc ataatgatag taggaggctt ggtaggttta agaatagttt      3660

ttgctgtact ttctgtagtg aatagagtta ggcagggata ttcaccatta tcgtttcaga      3720

cccacctccc aatcccgagg ggacccgaca ggcccgaagg aatagaagaa gaaggtggag      3780

agagagacag agacagatcc attcgattag tgaacggatc cttagcactt atctggtaa       3839


<210> 53
<211> 1101
<212> PRT
<213> Artificial sequence

<220>
<223> Modified Env/Tat

<400> 53

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
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Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
            20              25              30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35              40              45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50              55              60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65              70              75              80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
            85              90              95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100             105             110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Gly
        115             120             125

Ala Gly Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
    130             135             140

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
145             150             155             160

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
            165             170             175

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
            180             185             190

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
        195             200             205

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
    210             215             220

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
225             230             235             240

Lys Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile
                245                     250                 255

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Leu Gly Cys Thr Arg
                260                     265                 270

Pro Asn Asn Asn Thr Arg Lys Ser Val Arg Ile Gly Pro Gly Gln Thr
                275                     280                 285

Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys
        290                     295                 300

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Arg Ile Gly Pro
305                     310                 315                 320

Gly Gln Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln
                325                     330                 335

Ala His Cys Cys Thr Arg Pro Tyr Asn Asn Ile Arg Gln Arg Thr Pro
                340                     345                 350

Ile Gly Leu Gly Gln Ala Leu Tyr Thr Thr Arg Arg Ile Glu Asp Ile
        355                     360                 365

Arg Arg Ala His Cys Cys Thr Arg Pro Ser Thr Asn Thr Arg Thr Ser
        370                     375                 380

Ile Arg Ile Gly Pro Gly Gln Val Phe Tyr Arg Thr Gly Asp Ile Thr
385                     390                 395                 400

Gly Asp Ile Arg Lys Ala Tyr Cys Gly Ser Cys Thr Arg Pro Asn Asn
                405                     410                 415

Asn Thr Arg Lys Arg Ile Ser Leu Gly Pro Gly Arg Val Phe Tyr Thr
                420                     425                 430

Ala Gly Glu Ile Ile Gly Asp Ile Arg Lys Ala His Cys Cys Thr Arg
        435                     440                 445

Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Phe Ala Pro Gly Gln Ala
        450                     455                 460

Leu Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys
465                     470                 475                 480

Leu Gly Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Val Arg Ile
            485                   490             495

Gly Pro Gly Gln Thr Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile
            500                   505             510

Arg Gln Ala His Cys Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser
            515             520             525

Ile Arg Ile Gly Pro Gly Gln Ala Phe Tyr Ala Thr Gly Glu Ile Ile
    530             535             540

Gly Asp Ile Arg Gln Ala His Cys Cys Thr Arg Pro Tyr Asn Asn Ile
545             550             555             560

Arg Gln Arg Thr Pro Ile Gly Leu Gly Gln Ala Leu Tyr Thr Thr Arg
            565             570             575

Arg Ile Glu Asp Ile Arg Arg Ala His Cys Cys Thr Arg Pro Ser Thr
            580             585             590

Asn Thr Arg Thr Ser Ile Arg Ile Gly Pro Gly Gln Val Phe Tyr Arg
            595             600             605

Thr Gly Asp Ile Thr Gly Asp Ile Arg Lys Ala Tyr Cys Gly Ser Cys
    610             615             620

Thr Arg Pro Asn Asn Asn Thr Arg Lys Arg Ile Ser Leu Gly Pro Gly
625             630             635             640

Arg Val Phe Tyr Thr Ala Gly Glu Ile Ile Gly Asp Ile Arg Lys Ala
            645             650             655

His Cys Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Phe
            660             665             670

Ala Pro Gly Gln Ala Leu Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
            675             680             685

Arg Gln Ala His Cys Leu Gly Asn Ile Ser Arg Ala Lys Trp Asn Asn
            690             695             700

Thr Leu Lys Gln Ile Asp Ser Lys Leu Arg Glu Gln Phe Gly Asn Asn
705             710             715             720

Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile Val
                725                 730                 735

Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr
                740                 745                 750

Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp Ser Thr Lys Gly
            755                 760                 765

Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu Pro Cys Arg Ile
        770                 775                 780

Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala
785                 790                 795                 800

Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu
                805                 810                 815

Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu Ser Glu Ile Phe
            820                 825                 830

Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr
        835                 840                 845

Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys
    850                 855                 860

Ala Lys Arg Arg Val Val Gln Thr Ser Ala Val Gly Ile Gly Ala Leu
865                 870                 875                 880

Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser
            885                 890                 895

Met Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln
            900                 905                 910

Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu
        915                 920                 925

Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala
    930                 935                 940

Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys
945                 950                 955                 960

Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp

Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu
        980                    985                    990

Trp Asp Arg Glu Ile Asn Asn Tyr  Thr Ser Leu Ile His  Ser Leu Ile
        995                    1000                   1005

Glu Glu  Ser Gln Asn Gln Gln  Glu Lys Asn Glu Gln  Glu Leu Leu
        1010                   1015                   1020

Glu Leu  Asp Lys Trp Ala Ser  Leu Trp Asn Trp Phe  Asn Ile Thr
        1025                   1030                   1035

Asn Trp  Leu Trp Tyr Ile Lys  Leu Phe Ile Met Ile  Val Gly Gly
        1040                   1045                   1050

Leu Val  Gly Leu Arg Ile Val  Phe Ala Thr His Leu  Pro Ile Pro
        1055                   1060                   1065

Arg Gly  Pro Asp Arg Pro Glu  Gly Ile Glu Glu Glu  Gly Gly Glu
        1070                   1075                   1080

Arg Asp  Arg Asp Arg Ser Ile  Arg Leu Val Asn Gly  Ser Leu Ala
        1085                   1090                   1095

Leu Ile  Trp
        1100


<210>  54
<211>  4040
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Modified Env/Tat/Rev

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ggcgttactc gacagaggag agcaagaaat ggagccagta gatcctagac tagagccctg     120

gaagcatcca ggaagtcagc ctaaaactgc ttgtaccaat tgctattgta aaaagtgttg     180

ctttcattgc caagtttgtt tcataacaaa agccttaggc atctcctatg caggaagaa      240

gcggagacag cgacgaagac ctcctcaagg cagtcagact catcaagttt ctctatcaaa     300

gcagtaagta gtacatgtaa tgcaacctat acaaatagca atagtagcat tagtagtagc     360

aataataata gcaatagttg tgtggtccat agtaatcata gaatatagga aaatattaag     420

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acaaagaaaa atagacaggt taattgatag actaatagaa agagcagaag acagtggcaa      480

tgagagtgaa ggagaaatat cagcacttgt ggagatgggg gtggagatgg ggcaccatgc      540

tccttgggat gttgatgatc tgtagtgcta cagaaaaatt gtgggtcaca gtctattatg      600

gggtacctgt gtggaaggaa gcaaccacca ctctattttg tgcatcagat gctaaagcat      660

atgatacaga ggtacataat gtttgggcca cacatgcctg tgtacccaca gaccccaacc      720

cacaagaagt agtattggta aatgtgacag aaaattttaa catgtggaaa aatgacatgg      780

tagaacagat gcatgaggat ataatcagtt tatgggatca aagcctaaag ccatgtgtaa      840

aattaacccc actctgtgtt ggagctggta gttgtaacac ctcagtcatt acacaggcct      900

gtccaaaggt atcctttgag ccaattccca tacattattg tgccccggct ggttttgcga      960

ttctaaaatg taataataag acgttcaatg gaacaggacc atgtacaaat gtcagcacag     1020

tacaatgtac acatggaatt aggccagtag tatcaactca actgctgtta aatggcagtc     1080

tggcagaaga agaggtagta attagatctg ccaatttcac agacaatgct aaaaccataa     1140

tagtacagct gaaccaatct gtagaaatta attgtacaag acccaacaac aatacaagaa     1200

aaagtatccg tatccagaga ggaccaggga gagcatttgt tacaatagga aaaataggaa     1260

atatgagaca agcacattgt ctcgggtgta ccagacctaa caacaataca agaaaaagtg     1320

tacgtatagg accaggacaa acattctatg caacaggtga tataataggg gatataagac     1380

aagcacattg ttgtacgaga cccaacaata atacaagaaa aagtataagg ataggaccag     1440

gacaagcatt ctatgcaaca ggagaaataa taggagatat aagacaagca cattgttgca     1500

caaggcccta caacaatata agacaaagga cccccatagg actagggcaa gcactctata     1560

caacaagaag aatagaagat ataagaagag cacattgttg taccagaccc tccaccaata     1620

caagaacaag tatacgtata ggaccaggac aagtattcta tagaacagga gacataacag     1680

gagatataag aaaagcatat tgtggatcct gtacaagacc caacaacaat acaagaaaaa     1740

gaatatcttt aggaccagga cgagtatttt atacagcagg agaaataata ggagacatca     1800

gaaaggcaca ttgttgtacc agacctaata caatacaag aaaaagtata acttttgcac      1860

caggacaagc gctctatgca acaggtgaaa taataggaga tataagacaa gcacattgtc     1920

tcgggtgtac cagacctaac aacaatacaa gaaaaagtgt acgtatagga ccaggacaaa     1980

cattctatgc aacaggtgat ataataggg atataagaca agcacattgt tgtacgagac      2040

ccaacaataa tacaagaaaa agtataagga taggaccagg acaagcattc tatgcaacag     2100

gagaaataat aggagatata agacaagcac attgttgcac aaggccctac aacaatataa     2160

gacaaaggac ccccatagga ctagggcaag cactctatac aacaagaaga atagaagata     2220
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taagaagagc acattgttgt accagaccct ccaccaatac aagaacaagt atacgtatag    2280

gaccaggaca agtattctat agaacaggag acataacagg agatataaga aaagcatatt    2340

gtggatcctg tacaagaccc aacaacaata caagaaaaag aatatcttta ggaccaggac    2400

gagtatttta tacagcagga gaaataatag gagacatcag aaaggcacat tgttgtacca    2460

gacctaataa caatacaaga aaaagtataa cttttgcacc aggacaagcg ctctatgcaa    2520

caggtgaaat aataggagat ataagacaag cacattgtct cgggaacatt agtagagcaa    2580

aatggaataa cactttaaaa cagatagata gcaaattaag agaacaattt ggaaataata    2640

aaacaataat ctttaagcag tcctcaggag gggacccaga aattgtaacg cacagtttta    2700

attgtggagg ggaatttttc tactgtaatt caacacaact gtttaatagt acttggttta    2760

atagtacttg gagtactaaa gggtcaaata acactgaagg aagtgacaca atcaccctcc    2820

catgcagaat aaaacaaatt ataaacatgt ggcaggaagt aggaaaagca atgtatgccc    2880

ctcccatcag tggacaaatt agatgttcat caaatattac agggctgcta ttaacaagag    2940

atggtggtaa tagcaacaat gagtccgaga tcttcagacc tggaggagga gatatgaggg    3000

acaattggag aagtgaatta tataaatata agtagtaaa aattgaacca ttaggagtag    3060

cacccaccaa ggcaaagaga agagtggtgc agactagtgc agtgggaata ggagctttgt    3120

tccttgggtt cttgggagca gcaggaagca ctatgggctg cacgtcaatg acgctgacgg    3180

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gaatcctggc tgtggaaaga tacctaaagg atcaacagct cctggggatt tggggttgct    3360

ctggaaaact catttgcacc actgctgtgc cttggaatgc tagttggagt aataaatctc    3420

tggaacagat ttggaataac atgacctgga tggagtggga cagagaaatt aacaattaca    3480

caagcttaat acactcctta attgaagaat cgcaaaacca gcaagaaaag aatgaacaag    3540

aattattgga attagataaa tgggcaagtt tgtggaattg gtttaacata acaaattggc    3600

tgtggtatat aaaaattattc ataatgatag taggaggctt ggtaggttta agaatagttt    3660

ttgctgtact ttctatagtg aatagagtta ggcagggata ttcaccatta tcgtttcaga    3720

cccacctccc aatcccgagg ggacccgaca ggcccgaagg aatagaagaa gaaggtggag    3780

agagagacag agacagatcc attcgattag tgaacggatc cttagcactt atctgggacg    3840

atctgcggag cctgtgcctc ttcagctacc accgcttgag agacttactc ttgattgtaa    3900

cgaggattgt ggaacttctg ggacgcaggg ggtgggaagc cctcaaatat tggtggaatc    3960

tcctacagta ttggagtcag gaactaaaga atagtgctgt taacttgctc aatgccacag    4020

ccatagcagt agctgagtaa                                                  4040
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<210> 55
<211> 1186
<212> PRT
<213> Artificial sequence

<220>
<223> Modified Env/Tat/Rev

<400> 55

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                20                  25                  30


Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
            35                  40                  45


Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
        50                  55                  60


Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80


Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95


Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
                100                 105                 110


Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Gly
            115                 120                 125


Ala Gly Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
        130                 135                 140


Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
145                 150                 155                 160


Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
                165                 170                 175


Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
                180                 185                 190


Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
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Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
    210                 215                 220

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
225                 230                 235                 240

Lys Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile
              245                 250                 255

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Leu Gly Cys Thr Arg
          260                 265                 270

Pro Asn Asn Asn Thr Arg Lys Ser Val Arg Ile Gly Pro Gly Gln Thr
    275                 280                 285

Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys
    290                 295                 300

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Arg Ile Gly Pro
305                 310                 315                 320

Gly Gln Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln
              325                 330                 335

Ala His Cys Cys Thr Arg Pro Tyr Asn Asn Ile Arg Gln Arg Thr Pro
          340                 345                 350

Ile Gly Leu Gly Gln Ala Leu Tyr Thr Thr Arg Arg Ile Glu Asp Ile
    355                 360                 365

Arg Arg Ala His Cys Cys Thr Arg Pro Ser Thr Asn Thr Arg Thr Ser
    370                 375                 380

Ile Arg Ile Gly Pro Gly Gln Val Phe Tyr Arg Thr Gly Asp Ile Thr
385                 390                 395                 400

Gly Asp Ile Arg Lys Ala Tyr Cys Gly Ser Cys Thr Arg Pro Asn Asn
              405                 410                 415

Asn Thr Arg Lys Arg Ile Ser Leu Gly Pro Gly Arg Val Phe Tyr Thr
          420                 425                 430

Ala Gly Glu Ile Ile Gly Asp Ile Arg Lys Ala His Cys Cys Thr Arg
    435                 440                 445

```
Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Phe Ala Pro Gly Gln Ala
    450                 455                 460

Leu Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys
465                 470                 475                 480

Leu Gly Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Val Arg Ile
            485                 490                 495

Gly Pro Gly Gln Thr Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile
            500                 505                 510

Arg Gln Ala His Cys Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser
        515                 520                 525

Ile Arg Ile Gly Pro Gly Gln Ala Phe Tyr Ala Thr Gly Glu Ile Ile
    530                 535                 540

Gly Asp Ile Arg Gln Ala His Cys Cys Thr Arg Pro Tyr Asn Asn Ile
545                 550                 555                 560

Arg Gln Arg Thr Pro Ile Gly Leu Gly Gln Ala Leu Tyr Thr Thr Arg
            565                 570                 575

Arg Ile Glu Asp Ile Arg Arg Ala His Cys Cys Thr Arg Pro Ser Thr
            580                 585                 590

Asn Thr Arg Thr Ser Ile Arg Ile Gly Pro Gly Gln Val Phe Tyr Arg
        595                 600                 605

Thr Gly Asp Ile Thr Gly Asp Ile Arg Lys Ala Tyr Cys Gly Ser Cys
    610                 615                 620

Thr Arg Pro Asn Asn Asn Thr Arg Lys Arg Ile Ser Leu Gly Pro Gly
625                 630                 635                 640

Arg Val Phe Tyr Thr Ala Gly Glu Ile Ile Gly Asp Ile Arg Lys Ala
            645                 650                 655

His Cys Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Phe
            660                 665                 670

Ala Pro Gly Gln Ala Leu Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
        675                 680                 685
```

```
Arg Gln Ala His Cys Leu Gly Asn Ile Ser Arg Ala Lys Trp Asn Asn
    690                 695                 700

Thr Leu Lys Gln Ile Asp Ser Lys Leu Arg Glu Gln Phe Gly Asn Asn
705                 710                 715                 720

Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile Val
                725                 730                 735

Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr
            740                 745                 750

Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp Ser Thr Lys Gly
        755                 760                 765

Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu Pro Cys Arg Ile
    770                 775                 780

Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala
785                 790                 795                 800

Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu
            805                 810                 815

Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu Ser Glu Ile Phe
            820                 825                 830

Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr
        835                 840                 845

Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys
    850                 855                 860

Ala Lys Arg Arg Val Val Gln Thr Ser Ala Val Gly Ile Gly Ala Leu
865                 870                 875                 880

Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Cys Thr Ser
            885                 890                 895

Met Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Asp Ile Val Gln
            900                 905                 910

Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu
    915                 920                 925
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Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala
    930                 935                 940

Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys
945                 950                 955                 960

Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp
                965                 970                 975

Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu
            980                 985                 990

Trp Asp Arg Glu Ile Asn Asn Tyr  Thr Ser Leu Ile His  Ser Leu Ile
        995                 1000                1005

Glu Glu  Ser Gln Asn Gln Gln  Glu Lys Asn Glu Gln  Glu Leu Leu
    1010                1015                1020

Glu Leu  Asp Lys Trp Ala Ser  Leu Trp Asn Trp Phe  Asn Ile Thr
    1025                1030                1035

Asn Trp  Leu Trp Tyr Ile Lys  Leu Phe Ile Met Ile  Val Gly Gly
    1040                1045                1050

Leu Val  Gly Leu Arg Ile Val  Phe Ala Val Leu Ser  Ile Val Asn
    1055                1060                1065

Arg Val  Arg Gln Gly Tyr Ser  Pro Leu Ser Phe Gln  Thr His Leu
    1070                1075                1080

Pro Ile  Pro Arg Gly Pro Asp  Arg Pro Glu Gly Ile  Glu Glu Glu
    1085                1090                1095

Gly Gly  Glu Arg Asp Arg Asp  Arg Ser Ile Arg Leu  Val Asn Gly
    1100                1105                1110

Ser Leu  Ala Leu Ile Trp Asp  Asp Leu Arg Ser Leu  Cys Leu Phe
    1115                1120                1125

Ser Tyr  His Arg Leu Arg Asp  Leu Leu Leu Ile Val  Thr Arg Ile
    1130                1135                1140

Val Glu  Leu Leu Gly Arg Arg  Gly Trp Glu Ala Leu  Lys Tyr Trp
    1145                1150                1155

Trp Asn  Leu Leu Gln Tyr Trp  Ser Gln Glu Leu Lys  Asn Ser Ala
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          1160                1165                1170


      Val Asn  Leu Leu Asn Ala Thr  Ala Ile Ala Val Ala  Glu
         1175                1180                1185
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<210> 56
<211> 507
<212> DNA
<213> Human immunodeficiency virus type 1

<400> 56

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atgttcttta gggaagatct ggccttccta caagggaagg ccagggaatt ttcttcagag     60

cagaccagag ccaacagccc caccatttct tcagagcaga ccagagccaa cagccccacc    120

agaagagagc ttcaggtctg gggtagagac aacaactccc cctcagaagc aggagccgat    180

agacaaggaa ctgtatcctt taacttccct cagatcactc tttggcaacg acccctcgtc    240

acaataaaga tagggggggca actaaaggaa gctctattag atacaggagc agatgataca    300

gtattagaag aaatgagttt gccaggaaga tggaaaccaa aaatgatagg gggaattgga    360

ggttttatca agtaagaca gtatgatcag atactcatag aaatctgtgg acataaagct    420

ataggtacag tattagtagg acctacacct gtcaacataa ttggaagaaa tctgttgact    480

cagattggtt gcactttaaa tttttaa                                        507
```

<210> 57
<211> 168
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 57

```
Met Phe Phe Arg Glu Asp Leu Ala Phe Leu Gln Gly Lys Ala Arg Glu
1               5                   10                  15


Phe Ser Ser Glu Gln Thr Arg Ala Asn Ser Pro Thr Ile Ser Ser Glu
            20                  25                  30


Gln Thr Arg Ala Asn Ser Pro Thr Arg Arg Glu Leu Gln Val Trp Gly
            35                  40                  45


Arg Asp Asn Asn Ser Pro Ser Glu Ala Gly Ala Asp Arg Gln Gly Thr
    50                  55                  60


Val Ser Phe Asn Phe Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val
65                  70                  75                  80


Thr Ile Lys Ile Gly Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly
                85                  90                  95
```

Ala Asp Asp Thr Val Leu Glu Glu Met Ser Leu Pro Gly Arg Trp Lys
        100                 105                 110

Pro Lys Met Ile Gly Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr
        115                 120                 125

Asp Gln Ile Leu Ile Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val
    130                 135                 140

Leu Val Gly Pro Thr Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr
145                 150                 155                 160

Gln Ile Gly Cys Thr Leu Asn Phe
                165


<210> 58
<211> 1800
<212> DNA
<213> Artificial sequence

<220>
<223> Gag-PI

<400> 58
atgggtgcga gagcgtcagt attaagcggg ggagaattag atcgatggga aaaaattcgg      60

ttaaggccag ggggaaagaa aaaatataaa ttaaaacata tagtatgggc aagcagggag     120

ctagaacgat tcgcagttaa tcctggcctg ttagaaacat cagaaggctg tagacaaata     180

ctgggacagc tacaaccatc ccttcagaca ggatcagaag aacttagatc attatataat     240

acagtagcaa ccctctattg tgtgcatcaa aggatagaga taaaagacac caaggaagct     300

ttagacaaga tagaggaaga gcaaaacaaa agtaagaaaa agcacagca agcagcagct     360

gacacaggac acagcagtca ggtcagccaa aattacccta tagtgcagaa catccagggg     420

caaatggtac atcaggccat atcacctaga actttaaatg catgggtaaa agtagtagaa     480

gagaaggctt tcagcccaga agtaataccc atgttttcag cattatcaga aggagccacc     540

ccacaagatt taaacaccat gctaaacaca gtggggggac atcaagcagc catgcaaatg     600

ttaaaagaga ccatcaatga ggaagctgca gaatgggata gagtacatcc agtgcatgca     660

gggcctattg caccaggcca gatgagagaa ccaaggggaa gtgacatagc aggaactact     720

agtacccttc aggaacaaat aggatggatg acaaataatc cacctatccc agtaggagaa     780

atttataaaa gatggataat cctgggatta aataaaatag taagaatgta tagccctacc     840

agcattctgg acataagaca aggaccaaaa gaacctttta gagactatgt agaccggttc     900

```
tataaaactc taagagccga gcaagcttca caggaggtaa aaaattggat gacagaaacc      960

ttgttggtcc aaaatgcgaa cccagattgt aagactattt taaaagcatt gggaccagcg     1020

gctacactag aagaaatgat gacagcatgt cagggagtag gaggacccgg ccataaggca     1080

agagttttgg ctgaagcaat gagccaagta acaaatacag ctaccataat gatgcagaga     1140

ggcaattttta ggaaccaaag aaagatggtt aagtgtttca attgtggcaa agaagggcac     1200

acagccagaa attgcagggc ccctaggaaa aagggctgtt ggaaatgtgg aaaggaagga     1260

caccaaatga aagattgtac tgagagacag gctaatttct ttagggaaga tctggccttc     1320

ctacaaggga aggccaggga attttcttca gagcagacca gagccaacag ccccaccatt     1380

tcttcagagc agaccagagc aacagcccc accagaagag agcttcaggt ctggggtaga     1440

gacaacaact ccccctcaga agcaggagcc gatagacaag gaactgtatc ctttaacttc     1500

cctcagatca ctctttggca acgacccctc gtcacaataa agatagggg gcaactaaag     1560

gaagctctat tagatacagg agcagatgat acagtattag aagaaatgag tttgccagga     1620

agatggaaac caaaaatgat aggggggaatt ggaggtttta tcaaagtaag acagtatgat     1680

cagatactca tagaaatctg tggacataaa gctataggta cagtattagt aggacctaca     1740

cctgtcaaca taattggaag aaatctgttg actcagattg gttgcacttt aaattttaa     1800


<210>  59
<211>  599
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Gag-PI

<400>  59

Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp
1               5                   10                  15


Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
                20                  25                  30


His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
            35                  40                  45


Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
        50                  55                  60


Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
65                  70                  75                  80
```

```
Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
            85                  90                  95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
            100                 105                 110

Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val
            115                 120                 125

Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His
            130                 135                 140

Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
145                 150                 155                 160

Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser
            165                 170                 175

Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly
            180                 185                 190

Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu
            195                 200                 205

Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala
    210                 215                 220

Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr
225                 230                 235                 240

Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile
            245                 250                 255

Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys
            260                 265                 270

Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly
            275                 280                 285

Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
            290                 295                 300

Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr
305                 310                 315                 320

Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala
```

```
                  325                     330                     335


Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly
        340                 345                 350

Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser
        355                 360                 365

Gln Val Thr Asn Thr Ala Thr Ile Met Met Gln Arg Gly Asn Phe Arg
        370                 375                 380

Asn Gln Arg Lys Met Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His
385                 390                 395                 400

Thr Ala Arg Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys
        405                 410                 415

Gly Lys Glu Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn
        420                 425                 430

Phe Phe Arg Glu Asp Leu Ala Phe Leu Gln Gly Lys Ala Arg Glu Phe
        435                 440                 445

Ser Ser Glu Gln Thr Arg Ala Asn Ser Pro Thr Ile Ser Ser Glu Gln
        450                 455                 460

Thr Arg Ala Asn Ser Pro Thr Arg Arg Glu Leu Gln Val Trp Gly Arg
465                 470                 475                 480

Asp Asn Asn Ser Pro Ser Glu Ala Gly Ala Asp Arg Gln Gly Thr Val
        485                 490                 495

Ser Phe Asn Phe Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr
        500                 505                 510

Ile Lys Ile Gly Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala
        515                 520                 525

Asp Asp Thr Val Leu Glu Glu Met Ser Leu Pro Gly Arg Trp Lys Pro
530                 535                 540

Lys Met Ile Gly Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp
545                 550                 555                 560

Gln Ile Leu Ile Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu
        565                 570                 575
```

Val Gly Pro Thr Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln
        580                  585                  590

Ile Gly Cys Thr Leu Asn Phe
        595


<210>  60
<211>  51
<212>  DNA
<213>  Artificial sequence

<220>
<223>  PCR primer

<400>  60
aaatcaaccg gaattgaatt ccctcgggtg taccagacct aacaacaata c          51


<210>  61
<211>  42
<212>  DNA
<213>  Artificial sequence

<220>
<223>  PCR primer

<400>  61
attgttgggt ctcgtacaac aatgtgcttg tcttatatcc cc          42


<210>  62
<211>  41
<212>  DNA
<213>  Artificial sequence

<220>
<223>  PCR primer

<400>  62
ggggatataa gacaagcaca ttgtacgaga cccaacaata c          41


<210>  63
<211>  39
<212>  DNA
<213>  Artificial sequence

<220>
<223>  PCR primer

<400>  63
gttgtagggc cttgtgcaac aatgtgcttg tcttatatc          39


<210>  64
<211>  39
<212>  DNA

<213> Artificial sequence

<220>
<223> PCR primer

<400> 64
gatataagac aagcacattg ttgcacaagg ccctacaac                    39


<210> 65
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer

<400> 65
ggtggagggt ctggtacaac aatgtgctct tcttat                       36


<210> 66
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer

<400> 66
ataagaagag cacattgttg taccagaccc tccacc                       36


<210> 67
<211> 47
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer

<400> 67
gtattgttgt tgggtcttgt acaacaatat gcttttctta tatctcc           47


<210> 68
<211> 47
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer

<400> 68
ggagatataa gaaaagcata ttgttgtaca agacccaaca acaatac           47


<210> 69
<211> 39
<212> DNA
<213> Artificial sequence

```
<220>
<223>  PCR primer

<400>  69
gttattaggt ctggtacaac aatgtgcctt tctgatgtc                              39


<210>  70
<211>  39
<212>  DNA
<213>  Artificial sequence

<220>
<223>  PCR primer

<400>  70
gacatcagaa aggcacattg ttgtaccaga cctaataac                              39


<210>  71
<211>  54
<212>  DNA
<213>  Artificial sequence

<220>
<223>  PCR primer

<400>  71
aataaactag tctagacccc cgagtctaga acaatgtgct tgtcttatat ctcc            54


<210>  72
<211>  7
<212>  DNA
<213>  Artificial sequence

<220>
<223>  MMLV SD site

<400>  72
aggtaag                                                                 7


<210>  73
<211>  9
<212>  DNA
<213>  Artificial sequence

<220>
<223>  MMLV SA site

<400>  73
ctgctgcag                                                               9


<210>  74
<211>  90
<212>  DNA
<213>  Artificial sequence
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<220>
<223> DNA encoding gp120 signal peptide

<400> 74
atgagagtga aggagaaata tcagcacttg tggagatggg ggtggagatg gggcaccatg      60

ctccttggga tgttgatgat ctgtagtgct      90


<210> 75
<211> 129
<212> DNA
<213> Artificial sequence

<220>
<223> DNA encoding gp41 transmembrane domain

<400> 75
ttattcataa tgatagtagg aggcttggta ggtttaagaa tagttttgc tgtactttct      60

gtagtgaata gagttaggca gggatattca ccattatcgt ttcagaccca cctcccaatc     120

ccgagggga     129